

SEQUENCE LISTING

<110> Duvick, Jonathan P.
 Gilliam, Jacob T.
 Maddox, Joyce R.

<120> Amino Polyol Amine Oxidase
 Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134C

<150> US 60/092,936

<151> 1998-07-15

<150> US 60/135,391

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

<150> US 09/352,168

<151> 1999-07-12

<160> 53

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 372

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> misc_feature

<222> (346)...(346)

<223> n = A,T,C or G

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gcttggaactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc	120
attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatgggggtca cagctcgatt	180
ggaggacgcc cgagaagcct tgctcgcgcc accacggctt gtcccatacg aagactatct	240
tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg	300
gtgaaaatgt caaggtggga tacaagggtg tcggtaacga aaccancacc tttttgcttc	360
ggaacacggc gc	372

<210> 2

<211> 182

<212> DNA

<213> *Exophiala spinifera*

<400> 2

gaattttccg ccaatgcttg cttctcggcg ggaagaggtg gtgaaaatgt caaggtggga	60
tacaagggtg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc	120
gacgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc	180
ac	182

<210> 3

<211> 29

<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 3

tggtttcggt accgacaacc ttgtatccc

29

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 5' RACE, 21968

<400> 4

gagttggtcc cagacagact tttgtcgt

28

<210> 5

<211> 1389

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> CDS

<222> (1) ... (1386)

<400> 5

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Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
1 5 10 15

48

gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
20 25 30

96

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

144

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

192

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

240

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

288

ggc aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

336

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile

384

115	120	125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg 130 135 140			432
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu 145 150 155 160			480
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly 165 170 175			528
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180 185 190			576
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195 200 205			624
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met 210 215 220			672
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala 225 230 235 240			720
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly 245 250 255			768
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu 260 265 270			816
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala 275 280 285			864
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val 290 295 300			912
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln 305 310 315 320			960
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val 325 330 335			1008
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg 340 345 350			1056
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp			1104

355	360	365	
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg			1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro			
370	375	380	
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga			1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly			
385	390	395	400
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg			1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser			
	405	410	415
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg			1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr			
	420	425	430
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa			1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln			
	435	440	445
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca			1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
	450	455	460
tag			1389
<210> 6			
<211> 462			
<212> PRT			
<213> <i>Exophiala spinifera</i>			
<400> 6			
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1 5 10 15			
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu			
20 25 30			
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly			
35 40 45			
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp			
50 55 60			
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu			
65 70 75 80			
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp			
85 90 95			
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
100 105 110			
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile			
115 120 125			
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg			
130 135 140			
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
145 150 155 160			
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly			
165 170 175			
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys			
180 185 190			
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly			
195 200 205			
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met			

210	215	220
Ser Lys Glu Leu Val	Pro Gly Ser Val His	Leu Asn Thr Pro Val Ala
225	230	235
Glu Ile Glu Gln Ser	Ala Ser Gly Cys Thr	Val Arg Ser Ala Ser Gly
	245	250
Ala Val Phe Arg Ser	Lys Lys Val Val Val	Ser Leu Pro Thr Thr Leu
	260	265
Tyr Pro Thr Leu Thr	Phe Ser Pro Pro Leu	Pro Ala Glu Lys Gln Ala
	275	280
Leu Ala Glu Asn Ser	Ile Leu Gly Tyr Tyr	Ser Lys Ile Val Phe Val
	290	295
Trp Asp Lys Pro Trp	Trp Arg Glu Gln Gly	Phe Ser Gly Val Leu Gln
305	310	315
Ser Ser Cys Asp Pro	Ile Ser Phe Ala Arg	Asp Thr Ser Ile Asp Val
	325	330
Asp Arg Gln Trp Ser	Ile Thr Cys Phe Met	Val Gly Asp Pro Gly Arg
	340	345
Lys Trp Ser Gln Gln	Ser Lys Gln Val Arg	Gln Lys Ser Val Trp Asp
	355	360
Gln Leu Arg Ala Ala	Tyr Glu Asn Ala Gly	Ala Gln Val Pro Glu Pro
	370	375
Ala Asn Val Leu Glu	Ile Glu Trp Ser Lys	Gln Gln Tyr Phe Gln Gly
385	390	395
Ala Pro Ser Ala Val	Tyr Gly Leu Asn Asp	Leu Ile Thr Leu Gly Ser
	405	410
Ala Leu Arg Thr Pro	Phe Lys Ser Val His	Phe Val Gly Thr Glu Thr
	420	425
Ser Leu Val Trp Lys	Gly Tyr Met Glu Gly	Ala Ile Arg Ser Gly Gln
	435	440
Arg Gly Ala Ala Glu	Val Val Ala Ser Leu	Val Pro Ala Ala
450	455	460

<210> 7
 <211> 1442
 <212> DNA
 <213> *Exophiala spinifera*

<220>
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 <222> (1) ... (646)

<221> intron
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<221> CDS
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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192

Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	
50						55					60					
agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	240
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	
65					70					75					80	
ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	gac	288
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	
				85					90					95		
ggc	aca	acc	act	aca	gct	cct	tat	ggc	gac	tcc	ttg	ctg	agc	gag	gag	336
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	
			100					105					110			
gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	384
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	
		115					120					125				
gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	432
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	
	130					135					140					
ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	
145					150					155					160	
cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggc	528
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	
				165					170					175		
gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	
			180					185					190			
agt	gcc	acc	ggc	ctc	agt	aat	att	ttc	tgc	gac	aag	aaa	gac	ggc	ggg	624
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	
		195					200					205				
cag	tat	gtg	cga	tgc	aaa	aca	g	gtgcgtgtgg	tgctgtctca	ggcgggggac						676
Gln	Tyr	Val	Arg	Cys	Lys	Thr										
	210					215										
tcgtttctca	gtggcattc	cag	gt	atg	cag	tgc	att	tgc	cat	gcc	atg	tca				728
				Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser			
							220					225				
aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	776
Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	
				230					235					240		
att	gag	cag	tgc	gca	tcc	ggc	tgt	aca	gta	cga	tgc	gcc	tgc	ggc	gcc	824
Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	
			245					250					255			
gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tgc	tta	ccg	aca	acc	ttg	tat	872
Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	
		260					265					270				
ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	920
Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	

275	280	285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg			968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp			
290	295	300	305
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg			1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser			
	310	315	320
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat			1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp			
	325	330	335
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag			1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
	340	345	350
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa			1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
	355	360	365
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc			1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
	370	375	380
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct			1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
	390	395	400
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg			1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
	405	410	415
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct			1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			
	420	425	430
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga			1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			
	435	440	445
ggg gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			1442
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
	450	455	460

<210> 8

<211> 462

<212> PRT

<213> *Exophiala spinifera*

<400> 8

Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu			
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu			
	20	25	30
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly			
	35	40	45
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp			
	50	55	60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
 435 440 445
 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 9

<211> 458

<212> PRT

<213> Exophiala spinifera

<400> 9

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 20 25 30

Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
 210 215 220
 Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
 225 230 235 240
 Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
 245 250 255
 Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
 260 265 270
 Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
 275 280 285
 Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Arg Ser Lys
 290 295 300
 His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
 305 310 315 320
 Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
 325 330 335
 Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
 340 345 350
 Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
 355 360 365
 Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
 370 375 380
 Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
 385 390 395 400
 Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
 405 410 415
 Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
 420 425 430
 Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu
 435 440 445
 Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
 450 455

<210> 10
 <211> 1392
 <212> DNA
 <213> *Exophiala spinifera*
 <220>

<221> CDS

<222> (1)...(1389)

<221> misc_feature

<222> (1)...(3)

<223> Extra lysine in K:trAPAO

<400> 10

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672

Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala		
210						215				220							
atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc		720
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val		
225					230					235					240		
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg		768
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser		
				245					250					255			
ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc		816
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr		
			260					265					270				
ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa		864
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln		
		275					280					285					
gca	ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc		912
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe		
	290					295					300						
gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc		960
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu		
305					310					315					320		
caa	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac		1008
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp		
			325					330						335			
gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga		1056
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly		
			340					345					350				
cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg		1104
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp		
		355					360					365					
gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag		1152
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu		
	370					375					380						
ccg	gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa		1200
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln		
385					390					395					400		
gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt		1248
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly		
				405				410					415				
tcg	gcg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag		1296
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu		
			420					425					430				
acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt		1344
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly		
		435				440						445					
caa	cga	ggt	gct	gca	gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca			1389
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala			

450

455

460

tag

1392

<210> 11
 <211> 463
 <212> PRT
 <213> *Exophiala spinifera*

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 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly

	405		410		415										
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
			420					425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
		435					440						445		
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
	450					455					460				

<210> 12
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23256

<400> 12
 ggggaattca aagacaacgt tgcggacgtg gtag 34

<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23259

<400> 13
 ggggcggccg cctatgctgc tggcaccagg ctag 34

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
 tggtttcgtt accgacaacc ttgtatccc 29

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 5' race, N21968

<400> 15
 gagttggtcc cagacagact tttgtcgt 28

<210> 16
 <211> 1673
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> sig_peptide
 <222> (1)...(267)
 <223> yeast alpha mating factor secretion signal.

<221> CDS
 <222> (1)...(1662)

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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
                -85                      -80                      -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa      96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
                -70                      -65                      -60

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc     144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
                -55                      -50                      -45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg     192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
                -40                      -35                      -30

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta     240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
                -25                      -20                      -15

tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg     288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
                -5                      1                      5

gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc     336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
                10                      15                      20

aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat     384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
                25                      30                      35

cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg     432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
                40                      45                      50                      55

act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc     480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
                60                      65                      70

gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag     528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
                75                      80                      85

agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act     576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
                90                      95                      100

aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca     624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
                105                      110                      115

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ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 120 125 130 135	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 140 145 150	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 155 160 165	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 170 175 180	816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly 185 190 195	864
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg 200 205 210 215	912
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu 220 225 230	960
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln 235 240 245	1008
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg 250 255 260	1056
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu 265 270 275	1104
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn 280 285 290 295	1152
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro 300 305 310	1200
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp 315 320 325	1248
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp 330 335 340	1296
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln 345 350 355	1344
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca	1392

Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
 360 365 370 375

gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc 1440
 Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
 380 385 390

gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc 1488
 Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
 395 400 405

gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg 1536
 Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
 410 415 420

ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg 1584
 Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
 425 430 435

aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca 1632
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
 440 445 450 455

gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c 1673
 Glu Val Val Ala Ser Leu Val Pro Ala Ala
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<210> 17
 <211> 554
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> SIGNAL
 <222> (1)...(89)

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 -70 -65 -60
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
 -55 -50 -45
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -40 -35 -30
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -25 -20 -15 -10
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
 -5 1 5
 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
 10 15 20
 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
 25 30 35
 Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
 40 45 50 55
 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
 60 65 70
 Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
 75 80 85
 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr

	90		95		100										
Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala
	105					110					115				
Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser
120					125					130					135
Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val
			140					145						150	
Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu
		155						160					165		
Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His
	170					175						180			
Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly
185						190					195				
Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg
200					205					210					215
Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu
				220					225					230	
Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln
			235					240					245		
Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg
	250					255						260			
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu
265						270					275				
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn
280					285					290					295
Ser	Ile	Leu	Gly	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	
			300					305					310		
Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp
			315					320					325		
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp
	330					335						340			
Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln
	345				350					355					
Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala
360					365					370					375
Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu
			380						385					390	
Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala
			395					400					405		
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr
	410					415						420			
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp
	425					430					435				
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala
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Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala						
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<210> 18
 <211> 2079
 <212> DNA
 <213> Unknown

<220>

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
 - 687, gst fusion + polylinker, 688-2076,
 K:trAPAO, extra lysine underlined; 2077-2079, stop
 codon. For bacterial expression.

<221> CDS

<222> (1)...(2076)

<221> misc_feature

<222> (1)...(687)

<223> gst fusion + polylinker

<221> misc_feature

<222> (688)...(2076)

<223> K:trAPAO

<221> misc_feature

<222> (688)...(690)

<223> Extra lysine

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	

180							185							190							
ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc						624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala						
		195					200					205									
acg	ttt	ggg	ggg	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	gtt	ccg	cgt						672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg						
	210					215					220										
gga	tcc	ccg	gaa	ttc	aaa	gac	aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc						720
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly						
225					230					235					240						
gct	ggc	ttg	agc	ggg	ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggg						768
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly						
				245					250					255							
ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act						816
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr						
			260					265					270								
ctg	agc	gta	caa	tcg	ggg	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc						864
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly						
		275					280					285									
gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt						912
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe						
	290				295						300										
gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca						960
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser						
305				310				315						320							
atc	cat	caa	gca	caa	gac	ggg	aca	acc	act	aca	gct	cct	tat	ggg	gac						1008
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp						
				325				330						335							
tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc						1056
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro						
			340					345					350								
gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg						1104
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala						
		355				360						365									
agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt						1152
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys						
	370					375					380										
gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc						1200
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile						
385				390						395				400							
aca	cgc	gct	ctg	ctc	ggg	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt						1248
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe						
				405				410						415							
ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggg	ctc	agt	aat	att	ttc	tcg						1296
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser						
			420					425					430								

gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln 435 440 445	1344
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His 450 455 460	1392
ctc aac acc ccc gtc gct gaa att gag cag tgc gca tcc ggc tgt aca Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr 465 470 475 480	1440
gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val 485 490 495	1488
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu 500 505 510	1536
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr 515 520 525	1584
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly 530 535 540	1632
ttc tgc ggc gtc ctc caa tgc agc tgt gac ccc atc tca ttt gcc aga Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg 545 550 555 560	1680
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met 565 570 575	1728
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg 580 585 590	1776
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly 595 600 605	1824
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tgc aag Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys 610 615 620	1872
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp 625 630 635 640	1920
ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc aag agt gtt cat Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His 645 650 655	1968
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly 660 665 670	2016

gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg 2064
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 675 680 685

gtg cca gca gca tag 2079
 Val Pro Ala Ala
 690

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 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
 225 230 235 240
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
 245 250 255
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
 260 265 270
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
 275 280 285
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
 290 295 300
 Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
 305 310 315 320
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp
 325 330 335
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
 340 345 350
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
 355 360 365

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Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
370                               375                               380
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
385                               390                               395                               400
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
                               405                               410                               415
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
                               420                               425                               430
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
                               435                               440                               445
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
                               450                               455                               460
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
465                               470                               475                               480
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
                               485                               490                               495
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
                               500                               505                               510
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
                               515                               520                               525
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
530                               535                               540
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
545                               550                               555                               560
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
                               565                               570                               575
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
                               580                               585                               590
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
                               595                               600                               605
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
610                               615                               620
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
625                               630                               635                               640
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
                               645                               650                               655
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
                               660                               665                               670
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
675                               680                               685
Val Pro Ala Ala
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      fusion with barley alpha amylase signal sequence,
      for expression and secretion of the mature trAPAO
      in maize. Nucleotides 1-72, barley alpha amylase
      signal sequence, nucleotides 73-75, added lysine
      residue; nucleotides 76 -1464 , trAPAO cDNA.

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<223> Barley alpha amylase signal sequence

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<221> CDS
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-20 -15 -10	
ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta	96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val	
-5 1 5	
gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag	144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln	
10 15 20	
gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg	192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	
25 30 35 40	
gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg act atc aac	240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	
45 50 55	
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc	288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser	
60 65 70	
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act	336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr	
75 80 85	
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct	384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro	
90 95 100	
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa	432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu	
105 110 115 120	
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac	480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp	
125 130 135	
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg	528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	
140 145 150	
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca	576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala	
155 160 165	
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc	624

Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	
170						175					180					
atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggt	ctc	agt	aat	672
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	
185					190					195					200	
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Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	
				205					210					215		
ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	ggc	768
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	
			220					225					230			
tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	tcc	816
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	
		235					240					245				
ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	aag	864
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	
	250					255					260					
gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	tca	912
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	
265					270					275					280	
cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	tct	atc	ctg	960
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	
				285					290					295		
ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	cgc	1008
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	
			300					305					310			
gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	tca	1056
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	
		315					320					325				
ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	acc	1104
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	
	330					335					340					
tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	aag	1152
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	
345					350					355					360	
cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	gcc	tac	gag	1200
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	
				365				370						375		
aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	gag	1248
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	
			380					385					390			
tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	ggg	1296
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	
		395					400					405				
ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg	ctc	aga	acg	ccg	ttc	aag	1344
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	

410	415	420	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat			1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			
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atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg			1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val			
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gct agc ctg gtg cca gca gca tag			1464
Ala Ser Leu Val Pro Ala Ala			
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Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
	10				15					20					
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
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Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
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Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser
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Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
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Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
	90				95					100					
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
105				110					115						120
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
			125					130						135	
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala
			140				145					150			
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
		155				160					165				
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
	170				175					180					
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
185				190					195						200
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
			205					210						215	
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
			220					225					230		
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
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Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys
	250					255					260				

Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
 265 270 275 280
 Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
 285 290 295
 Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
 300 305 310
 Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
 315 320 325
 Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
 330 335 340
 Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
 345 350 355 360
 Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
 365 370 375
 Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
 380 385 390
 Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
 395 400 405
 Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
 410 415 420
 Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
 425 430 435 440
 Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
 445 450 455
 Ala Ser Leu Val Pro Ala Ala
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 <222> (1)...(1800)

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val 100 105 110	336
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala 115 120 125	384
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val 130 135 140	432
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 145 150 155 160	480
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 165 170 175	528
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 180 185 190	576
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195 200 205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 225 230 235 240	720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245 250 255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270	816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285	864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290 295 300	912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305 310 315 320	960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325 330 335	1008

aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa	1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	
340 345 350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca	1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	
355 360 365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca	1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
370 375 380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa	1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
385 390 395 400	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt	1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
405 410 415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc	1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
420 425 430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
435 440 445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc	1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
450 455 460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515 520 525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc	1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt	1776

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590

gtg gct agc ctg gtg cca gca gca tag
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

1803

<210> 23
 <211> 600
 <212> PRT
 <213> Exophiala spinifera

<400> 23

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 Thr Ile Ala Gly Gln Ile Gly Gln Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
 225 230 235 240
 Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
 260 265 270
 Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala

370		375		380
Ser Gly Cys Thr Val	Arg Ser Ala Ser Gly Ala	Val Phe Arg Ser Lys		
385	390	395	400	
Lys Val Val Val Ser	Leu Pro Thr Thr Leu Tyr Pro Thr	Leu Thr Phe		
	405	410	415	
Ser Pro Pro Leu Pro	Ala Glu Lys Gln Ala Leu Ala Glu	Asn Ser Ile		
	420	425	430	
Leu Gly Tyr Tyr Ser	Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
	435	440	445	
Arg Glu Gln Gly Phe	Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
	450	455	460	
Ser Phe Ala Arg Asp	Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
465	470	475	480	
Thr Cys Phe Met Val	Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
	485	490	495	
Lys Gln Val Arg Gln	Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
	500	505	510	
Glu Asn Ala Gly Ala	Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
	515	520	525	
Glu Trp Ser Lys Gln	Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
	530	535	540	
Gly Leu Asn Asp Leu	Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
545	550	555	560	
Lys Ser Val His Phe	Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
	565	570	575	
Tyr Met Glu Gly Ala	Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
	580	585	590	
Val Ala Ser Leu Val	Pro Ala Ala			
	595	600		

<210> 24

<211> 3003

<212> DNA

<213> Unknown

<220>

<223> Sequence is barley alpha amylase signal sequence:
 espl mat: an artificial spacer sequence and
 K:trAPAO

<221> sig_peptide

<222> (1)...(72)

<223> Barley alpha amylase signal sequence

<221> misc_feature

<222> (73)...(1575)

<223> espl mat

<221> misc_feature

<222> (1576)...(1611)

<223> spacer sequence

<221> misc_feature

<222> (1612)...(3000)

<223> K:trAPAO

<221> CDS

<222> (1)...(3000)

<221> misc_feature

<222> (1612)...(1614)

<223> Extra lysine

<400> 24

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ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct	96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala	
-5 1 5	
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc	144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr	
10 15 20	
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt	192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe	
25 30 35 40	
gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act	240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr	
45 50 55	
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc	288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu	
60 65 70	
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly	
75 80 85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca	624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720

Gly	Gly	Arg	Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro	
				205					210					215		
ccc	ttc	cga	gca	gca	atc	atg	gag	tcc	ggt	gtg	gct	aac	tac	aac	ttc	768
Pro	Phe	Arg	Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe	
			220					225					230			
ccc	aag	gga	gat	ttg	tcc	gaa	cct	tgg	aac	acc	act	gtt	caa	gct	ctc	816
Pro	Lys	Gly	Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu	
		235					240					245				
aac	tgt	acc	acc	agt	atc	gac	atc	ttg	agt	tgt	atg	aga	aga	gtc	gat	864
Asn	Cys	Thr	Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp	
	250					255					260					
ctc	gcc	act	ctg	atg	aac	acg	atc	gag	caa	ctc	gga	ctt	ggg	ttt	gag	912
Leu	Ala	Thr	Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu	
265					270					275					280	
tac	acg	ttg	gac	aac	gta	acg	gct	gtg	tac	cgt	tct	gaa	acg	gct	cgc	960
Tyr	Thr	Leu	Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg	
				285					290					295		
acg	act	ggt	gac	att	gct	cgt	gta	cct	gtt	ctc	gtc	ggg	acg	gtg	gcc	1008
Thr	Thr	Gly	Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala	
			300					305					310			
aac	gac	gga	ctt	ctc	ttt	gtc	ctc	ggg	gag	aat	gac	acc	caa	gca	tat	1056
Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr	
		315					320					325				
ctc	gag	gag	gca	atc	ccg	aat	cag	ccc	gac	ctt	tac	cag	act	ctc	ctt	1104
Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu	
	330					335					340					
gga	gca	tat	ccc	att	gga	tcc	cca	ggg	atc	gga	tcg	cct	caa	gat	cag	1152
Gly	Ala	Tyr	Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln	
345					350					355					360	
att	gcc	gcc	att	gag	acc	gag	gta	aga	ttc	cag	tgt	cct	tct	gcc	atc	1200
Ile	Ala	Ala	Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile	
				365				370						375		
gtg	gct	cag	gac	tcc	cgg	aat	cgg	ggt	atc	cct	tct	tgg	cgc	tac	tac	1248
Val	Ala	Gln	Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr	
			380					385					390			
tac	aat	gcg	acc	ttt	gag	aat	ctg	gag	ctt	ttc	cct	ggg	tcc	gaa	gtg	1296
Tyr	Asn	Ala	Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val	
		395					400					405				
tac	cac	agc	tct	gaa	gtc	ggg	atg	gtg	ttt	ggc	acg	tat	cct	gtc	gca	1344
Tyr	His	Ser	Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala	
	410					415					420					
agt	gcg	acc	gcc	ttg	gag	gcc	cag	acg	agc	aaa	tac	atg	cag	ggt	gcc	1392
Ser	Ala	Thr	Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala	
425					430					435					440	
tgg	gcg	gcc	ttt	gcc	aaa	aac	ccc	atg	aat	ggg	cct	ggg	tgg	aaa	caa	1440
Trp	Ala	Ala	Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln	

			445				450				455								
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Val	Pro	Asn	Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val				
			460				465				470								
gac	gtc	tct	cca	gcg	aca	ata	gac	caa	cga	tgt	gcc	ttg	tac	acg	cgt		1536		
Asp	Val	Ser	Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg				
			475				480				485								
tat	tat	act	gag	ttg	ggc	aca	atc	gcg	ccg	agg	aca	ttt	ggc	gga	ggc		1584		
Tyr	Tyr	Thr	Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly				
			490				495				500								
agc	ggc	gga	ggc	agc	ggc	gga	ggc	agc	aaa	gac	aac	gtt	gcg	gac	gtg		1632		
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp	Val				
			505				510				515				520				
gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc	aaa	gtc		1680		
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val				
			525				530				535								
cag	gcc	gcc	ggt	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta		1728		
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val				
			540				545				550								
ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg	act	atc		1776		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile				
			555				560				565								
aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta		1824		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val				
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Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr				
			585				590				595				600				
act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct		1920		
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala				
			605				610				615								
cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg		1968		
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala				
			620				625				630								
gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa		2016		
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln				
			635				640				645								
gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	agc	ttc		2064		
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe				
			650				655				660								
gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta		2112		
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val				
			665				670				675				680				
gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	gtg	gaa	gcc	cac	gag	atc		2160		
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile				
			685				690				695								

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Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	
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aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa	2256
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	
715 720 725	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca	2304
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	
730 735 740	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca	2352
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
745 750 755 760	
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Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
765 770 775	
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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
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Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
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Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
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Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
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Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
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Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
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Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
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Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
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Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
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445 450 455	

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Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	
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Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	
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Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	
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Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	
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Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	
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Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu	
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Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val	
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Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly	
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Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala	

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Gln	Phe	Gly	Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	
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Gly	Arg	Ala	Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	
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Gln	Phe	Asn	Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	
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Gly	Ala	Pro	Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	
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Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	
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Arg	Phe	Ala	Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	
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Ala	Tyr	Ser	Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	
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Ala	Ala	Val	Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	
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Ala	Lys	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	
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Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	
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Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	
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Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	
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Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
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Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Pro	Val	Trp	Ser	Gln	Leu		
			620					625					630			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	
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Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	
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Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	
665					670			</								

```

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
  810                      815                      820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                      830                      835                      840
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                      845                      850                      855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
                      860                      865                      870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
                      875                      880                      885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
                      890                      895                      900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                      910                      915                      920
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                      925                      930                      935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
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<210> 28
<211> 3618
<212> DNA
<213> Unknown

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<220>
<223> gst:esp1:sp:K:trapao, 3618. 1-687, gst +
polylinker; 688-2190, esp1 mat; 2191-2226 spacer;
2227-3615, K:trAPAO, 3616-3618, stop codon. For
bacterial expression.

```

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<221> CDS
<222> (1)...(3615)

<221> misc_feature
<222> (1)...(687)
<223> gst + polylinker

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<221> mat_peptide
<222> (688)...(2190)
<223> esp1 mat

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<221> misc_feature
<222> (2191)...(2226)
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<221> misc_feature
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<223> K:trAPAO

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<221> misc_feature
<222> (2227)...(2229)
<223> Extra lysine

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<400> 28

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  1                      5                      10                      15

```

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Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
tat	gag	cgc	gat	gaa	ggc	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
ggc	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggc	gat	gtt	aaa	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
	65				70					75					80	
atg	ttg	ggc	ggc	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
gga	gcg	gtt	ttg	gat	att	aga	tac	ggc	gtt	tcg	aga	att	gca	tat	agt	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
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Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
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Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
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Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
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gtt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
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Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
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Gly	Ser	Pro	Glu	Phe	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala	Gly	Met	Val	
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Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr	Val	Ser	Glu	
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Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe	Ala	Pro	Pro		
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Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu	Arg	Glu	Ile		
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Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu	Asn	Thr	Asn		
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Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu	Tyr	Gly	Trp		
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aat	tca	ttc	cac	ctt	tac	gac	ggg	gct	agt	ttc	gca	gcc	aat	cag	gat	1104	
Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala	Asn	Gln	Asp		
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Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu	Gly	Phe	Pro		
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gct	gcc	cct	cag	ctt	cca	ata	aca	cag	cga	aat	ctg	ggg	ttc	cta	gac	1200	
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Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala	Ala	Phe	Gly		
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Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala	Gly	Gly	Arg		
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agt	gtc	gac	gtc	ctc	ttg	acg	tct	atg	cca	cac	aac	cca	ccc	ttc	cga	1344	
Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro	Pro	Phe	Arg		
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Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu	Asn	Cys	Thr		
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acc	agt	atc	gac	atc	ttg	agt	tgt	atg	aga	aga	gtc	gat	ctc	gcc	act	1488	
Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp	Leu	Ala	Thr		
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ctg	atg	aac	acg	atc	gag	caa	ctc	gga	ctt	ggg	ttt	gag	tac	acg	ttg	1536	
Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu	Tyr	Thr	Leu		

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595				600				605								
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610				615				620								
acc Thr	ttt Phe	gag Glu	aat Asn	ctg Leu	gag Glu	ctt Leu	ttc Phe	cct Pro	ggg Gly	tcc Ser	gaa Glu	gtg Val	tac Tyr	cac His	agc Ser	1920
625				630				635				640				
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645				650				655								
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660				665				670								
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675				680				685								
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770 775 780	
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785 790 795 800	
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Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn	
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tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt	2544
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly	
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Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu	
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ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag	2640
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys	
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Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr	
885 890 895	
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Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln	
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Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu	
915 920 925	
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Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	
930 935 940	
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Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met	
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Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val	
965 970 975	
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt	2976
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys	
980 985 990	

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Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val	
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Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro	
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Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr	
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Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln	
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1125 1130 1135	
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Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn	
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Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
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Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
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Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
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Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
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Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu	Asn	Thr	Asn
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 Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly
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+ polylinker, 688-2163, BEST1 mature; 2164-2199,
spacer, 2200-3588, K:trAPAO

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
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tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
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Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
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Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
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			20					25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
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Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75				80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90					95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
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Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
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Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130					135					140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155				160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
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Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
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Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
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Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
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Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	Gly	Ile	Pro
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Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	Pro	Gln	His
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Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	Gly	Ser	Asp
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Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	Pro	Gly	Val
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Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	Gly	Ala	Lys
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Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly	Gly	Phe	Ala
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Gly	Gly	Thr	Ala	Ala	Met	Pro	Tyr	Tyr	Asp	Gly	Glu	Ala	Leu	Ala	Arg
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Gln	Gly	Val	Val	Val	Val	Thr	Phe	Asn	Tyr	Arg	Thr	Asn	Ile	Leu	Gly
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Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr	Gly	Thr	Ser
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Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	Trp	Val	Gln

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Gly Glu Ser Ala	Gly Ala Ser Ala Ile Gly	Leu Leu Leu Thr Ser Pro				
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Leu Ser Lys Gly	Leu Phe Arg Gly Ala Ile	Leu Glu Ser Pro Gly Leu				
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Thr Arg Pro Leu	Ala Thr Leu Ala Asp Ser	Ala Ala Ser Gly Glu Arg				
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Leu Asp Ala Asp	Leu Ser Arg Leu Arg Ser	Thr Asp Pro Ala Thr Leu				
465	470	475			480	
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Pro Arg Pro Thr	Gly Pro Ile Val Asp Gly	His Val Leu Pro Gln Thr				
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Asp Ser Ala Ala	Ile Ala Ala Gly Gln Leu	Ala Pro Val Arg Val Leu				
	515	520			525	
Ile Gly Thr Asn	Ala Asp Glu Gly Arg Ala	Phe Leu Gly Arg Ala Pro				
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Met Glu Thr Pro	Ala Asp Tyr Gln Ala Tyr	Leu Glu Ala Gln Phe Gly				
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Asp Gln Ala Ala	Ala Val Ala Ala Cys Tyr	Pro Leu Asp Gly Arg Ala				
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Thr Pro Lys Glu	Met Val Ala Arg Ile Phe	Gly Asp Asn Gln Phe Asn				
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Arg Gly Val Ser	Ala Phe Ser Glu Ala Leu	Val Arg Gln Gly Ala Pro				
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Val Trp Arg Tyr	Gln Phe Asn Gly Asn Thr	Glu Gly Arg Ala Pro				
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Ala Thr His Gly	Ala Glu Ile Pro Tyr Val	Phe Gly Val Phe Lys Leu				
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Asp Glu Leu Gly	Leu Phe Asp Trp Pro Pro	Glu Gly Pro Thr Pro Ala				
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Asp Arg Ala Leu	Gly Gln Leu Met Ser Ser	Ala Trp Val Arg Phe Ala				
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Lys Asn Gly Asp	Pro Ala Gly Asp Ala Leu	Thr Trp Pro Ala Tyr Ser				
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Thr Gly Lys Ser	Thr Met Thr Phe Gly Pro	Glu Gly Arg Ala Ala Val				
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Val Ser Pro Gly	Pro Ser Ile Pro Pro Cys	Ala Asp Gly Ala Lys Ala				
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Gly Gly Gly Gly	Ser Gly Gly Gly Ser Gly	Gly Gly Ser Lys Asp Asn				
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Val Ala Asp Val	Val Val Val Gly Ala Gly	Leu Ser Gly Leu Glu Thr				
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Ala Arg Lys Val	Gln Ala Ala Gly Leu Ser	Cys Leu Val Leu Glu Ala				
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Arg Thr Thr Ile	Asn Asp Leu Gly Ala Ala	Trp Ile Asn Asp Ser Asn				
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Gln Ser Glu Val	Ser Arg Leu Phe Glu Arg	Phe His Leu Glu Gly Glu				
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Leu Gln Arg Thr	Thr Gly Asn Ser Ile His	Gln Ala Gln Asp Gly Thr				
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Thr Thr Thr Ala	Pro Tyr Gly Asp Ser Leu	Leu Ser Glu Glu Val Ala				
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Ser Ala Leu Ala	Glu Leu Leu Pro Val Trp	Ser Gln Leu Ile Glu Glu				
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His Ser Leu Gln	Asp Leu Lys Ala Ser Pro	Gln Ala Lys Arg Leu Asp				
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Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
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 Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala
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 Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr
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 Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys
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 Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
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 Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
 980 985 990
 Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
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 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
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Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
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ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
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tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
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Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
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Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
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Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
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Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
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cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
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Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val	
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Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
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Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	
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Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	
245 250 255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa	816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln	
260 265 270	

gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc	864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe	
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gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta	912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val	
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Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile	
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Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	
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Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	
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aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca	1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	
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ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca	1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
370 375 380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa	1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
385 390 395 400	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt	1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
405 410 415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc	1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
420 425 430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
435 440 445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc	1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
450 455 460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
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gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat 1632
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
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 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
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 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
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 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
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 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
 195 200 205
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240
 Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala

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Thr	Ile	Ala 35	Gly	Gln	Ile	Gly	Gln 40	Asp	Ala	Leu	Gly 45	Val	Thr	Asp	Pro
Ala	Tyr 50	Glu	Lys	Gln	Val	Ala 55	Gln	Ala	Phe	Ala 60	Asn	Leu	Arg	Ala	Cys
Leu 65	Ala	Ala	Val	Gly 70	Ala	Ser	Ser	Asn	Asp 75	Val	Thr	Lys	Leu	Asn 80	Tyr
Tyr	Ile	Val	Asp 85	Tyr	Ala	Pro	Ser	Lys 90	Leu	Thr	Ala 95	Ile	Gly	Asp	Gly

Leu	Lys	Ser	Thr 100	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr 110	Leu	Val
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Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
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Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
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Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
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Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
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Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
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Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225					230					235					240
Pro	Tyr	Gly	Asp	Ser	Pro	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
				245					250					255	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	Tyr	Ser	Leu	Glu
			260					265					270		
Asp	Pro	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
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Ala	His	Tyr	Cys	Glu	Lys	Asp	Leu	Asn	Leu	Pro	Ala	Val	Leu	Ser	Val
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Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
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Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
				325					330					335	
Asn	Ile	Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
			340					345					350		
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro
		355					360					365			
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Gly	Ile	Glu	Gln	Ser	Ala
	370					375					380				
Ser	Gly	Cys	Ile	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys
385					390					395					400
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe
				405					410					415	
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Lys	Ser	Ile
			420					425					430		
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Asn	Pro	Trp	Trp
		435					440					445			
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys			

580
Val Ala Ser Leu Val Pro Ala Ala
595 600

585

590

<210> 37
<211> 1929
<212> DNA
<213> *Exophiala spinifera*

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1186)

<400> 37

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cacatcgggc	taggcccaca	cgaagcgagg	tatgtgacaa	tagctggaca	gattggacaa	120
gacgctttgg	gctgacaga	cccagcctac	gagaaacagg	ttgcccagc	attcgccaat	180
ctgcgagctt	gccttgctgc	agttggagcc	tcttcaaacy	acgtcaccaa	gctcaattac	240
tacatcgctc	actacgcccc	gagcaaaactc	accgcaattg	gagatgggct	gaagtctacc	300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccag	taccggcctt	ggcttcacct	360
gaatacctct	ttgaggttga	cggcacggcg	ctgggtgccag	gacactcgac	cccagacaac	420
gttgcggacg	tggtagtggg	gggcgctggc	ttgagcggct	tggagacggc	acgcaaagtc	480
caggccggcg	gtctgtcctg	cctcgcttct	gaggcgatgg	atcgtgtagg	gggaaagact	540
ctgagcgtag	aatcggggtc	cggcaggacg	actatcaacg	acctcggcgc	tgctgtggatc	600
aatgacagca	accaaagcga	agtatccaga	ttgtttgaaa	gatttcatth	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggtg	actccccggg	aagcacaaatc	ccactttgtg	atgagacctc	tgctgagtg	780
agaatacagt	cactgactcc	acttcgtcca	gctgagcgag	gaggttgcaa	gtgcacttgc	840
ggaactcctc	cccgtagtgt	ctcagctgat	cgaagagtat	agccttgaag	accccaaggc	900
gagccctcag	gcgaagcggc	tcgacagtgt	gagcttcgag	cactactgtg	agaaggacct	960
aaacttgctc	gctgttctca	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcga	ccggtctcag	1080
taatattgtc	tcggacaaga	aagacggcgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
cgggtgcctc	tcaggtaggg	gactcgtttc	ttagtgggtc	ttccagggtat	gcagtcgatt	1200
tgccatgcc	tgtcaaagga	acttggtcca	ggctcagtg	acctcaaac	ccccgtcgct	1260
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atagtcttcg	tatgggacaa	cccgtgggtg	cgcgaacaag	gcttctcggg	cgctctccaa	1500
tcgagctgtg	accccatctc	atttgccaga	gataccagca	tcgaagtcga	tcggcaatgg	1560
tcattacct	gtttcatggt	cggagaccgc	ggacgggaag	ggtcccaaca	gtccaagcag	1620
gtacgacaaa	agtctgtctg	ggaccaactc	cgcgcagcct	acgagaacgc	cggggcccaa	1680
gtcccagagc	cggccaacgt	gctcgaaatc	gagtggtcga	agcagcagta	tttccaagga	1740
gctccgagcg	ccgtctatgg	gctgaacgat	ctcatcacac	tgggttcggc	gctcagaacg	1800
ccgttcaagt	gtgttcattt	cgttgaacg	gagacgtctt	tagtttggaa	aggggtatatg	1860
gaaggggcca	tacgatcggg	tcaacgaggt	gctgcagaag	ttgtggctag	cctggtgcc	1920
gcagcatag						1929

<210> 38
<211> 600
<212> PRT
<213> *Exophiala spinifera*

<400> 38

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
			20					25					30		

Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65				70					75						80
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
				85					90					95	
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130				135						140				
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145				150						155					160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
				165					170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
		195					200					205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
	210					215					220				
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225				230						235					240
Pro	Tyr	Gly	Asp	Ser	Pro	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
				245					250					255	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	Tyr	Ser	Leu	Glu
			260					265					270		
Asp	Pro	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
		275					280					285			
Ala	His	Tyr	Cys	Glu	Lys	Asp	Leu	Asn	Leu	Pro	Ala	Val	Leu	Ser	Val
	290					295					300				
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
305				310						315					320
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
				325					330					335	
Asn	Ile	Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
			340					345					350		
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro
		355					360					365			
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Gly	Ile	Glu	Gln	Ser	Ala
	370					375					380				
Ser	Gly	Cys													

515	520	525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
530	535	540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
545	550	555
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		
	565	570
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		
	580	585
Val Ala Ser Leu Val Pro Ala Ala		590
595	600	

<210> 39
 <211> 1930
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1187)

<221> misc_feature
 <222> (648)...(648)
 <223> n = A,T,C or G

<400> 39

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gacgcttcgg	gcgtgacaga	ccctgcctac	gagaaacagg	ttgcccagc	attcgccaat	180
ctgcgagctt	gccttgctgc	agttggagcc	acttcaaacg	acgtcaccaa	gctcaattac	240
tacatcgctg	actacgcccc	gagcaaactc	accgcaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccag	tgctcgccctt	gtcttcacct	360
gaatacctct	ttgaggttga	tgccacggcg	ctgggtgccg	gacacacgac	cccagacaac	420
gttgcggaag	tggtagtggg	gggcgctggc	ttgagcgggt	tggagacggc	acgcaaagtc	480
caggccgcgc	gtctgtcctg	cctcgttctt	gaggcgatgg	atcggttagg	gggaaagact	540
ctgagcgta	aatcgggtcc	cggcaggacg	actatcaacg	acctcggcgc	tgctgtggatc	600
aatgacagca	accaaagcga	agtatccaga	ttgtttgaaa	gatttcatnt	ggagggcgag	660
ctccagagga	cgactggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggt	actccttggt	aagcacaatc	ccactttgtg	atgagacctc	tgctcagagt	780
agaatacagt	cactgattcc	acttcgtcca	gctgagcgag	gaggttgcaa	gtgcacttgc	840
ggaactcctc	cccgtatggt	ctcagctgat	cgaagagcat	agccttcaag	acctcaaggc	900
gagccctcag	gcgaagcggc	tcgacagtgt	gagcttcgcg	cactactgtg	agaaggaact	960
aaacttgcc	gctgttctcg	gcgtagcaaa	ccagatcaca	cgcgctctgc	tcgggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcc	ccggtctcag	1080
taatattttc	tcggacaaga	aagacggcgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
tggtgtcgtc	tcaggtgggg	gactcgtttc	tcaagtgggt	atttcaggta	tgcatcagat	1200
ttgccatgcc	atgtcaaaag	aacttgttcc	aggctcagtg	cacctcaaca	cccccgctgc	1260
tgaaattgag	cagtcggcat	ccggctgtac	agtacgatcg	gcctcggggc	ccgtgttccg	1320
aagcaaaaag	gtggtggttt	cgttaccgac	aaccttgat	cccaccttga	cattttcacc	1380
acctctcccc	gccgagaagc	aagcattggc	ggaaaattct	atcctgggct	actatagcaa	1440
gatagtcttc	gtatgggaca	agccgtgggt	gcgcgaacaa	ggcttctcgg	gcgtcctcca	1500
atcgagctgt	gaccccatct	catttgccag	agataccagc	atcgacgtcg	atcgacaatg	1560
gtccattacc	tgtttcatgg	tcggagaccc	gggacggaag	tggtcccaac	agtccaagca	1620
ggtacgacaa	aagtctgtct	gggaccaact	ccgcgcagcc	tacgagaacg	ccggggccca	1680
agtcacagag	ccggccaacg	tgctcgaat	cgagtggctg	aagcagcagt	atttccaagg	1740
agctccgag	gccgtctatg	ggctgaacga	tctcatcaca	ctgggttcgg	cgctcagaac	1800
gccgtttcaag	agtgttcatt	tcgttggaac	ggagacgtct	ttagtttgga	aagggtatat	1860
ggaaggggccc	atacgatcgg	gtcaacgagg	tgctgcagaa	gttgtggcta	gcctgggtgcc	1920

agcagcatag

1930

<210> 40
 <211> 598
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> VARIANT
 <222> (216)...(216)
 <223> Xaa = Any Amino Acid

<400> 40

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85						90					95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120						125		
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135						140			
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
145					150					155					160
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
			165						170					175	
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
			180					185						190	
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser
	195						200					205			
Arg	Leu	Phe	Glu	Arg	Phe	His	Xaa	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
	210				215						220				
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
225					230					235					240
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
			245						250					255	
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
		260					265						270		
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala
	275						280					285			
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Asn
	290					295					300				
Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met
305					310					315					320
Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile
			325						330					335	
Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly
		340				345							350		
Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser
	355						360					365			
Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly
	370					375					380				

Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val
 385 390 395 400
 Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro
 405 410 415
 Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly
 420 425 430
 Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
 435 440 445
 Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
 450 455 460
 Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys
 465 470 475 480
 Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
 485 490 495
 Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn
 500 505 510
 Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
 515 520 525
 Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu
 530 535 540
 Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser
 545 550 555 560
 Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
 565 570 575
 Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
 580 585 590
 Ser Leu Val Pro Ala Ala
 595

<210> 41
 <211> 1928
 <212> DNA
 <213> Rhinocycladiella atrovirens

<220>
 <221> intron
 <222> (739)...(811)
 <221> intron
 <222> (1134)...(1185)

<400> 41

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cacgtcggcg	taggccc aaa	cggagggagg	tatgcgacaa	tagctggaca	gattggacaa	120
gacgcttcgg	cogtgacaga	ccctgcctac	gagaaacagg	ttgccc aagc	attcgccaac	180
ctgcgagctt	gtcttgcctg	agttggagcc	acttcaa acg	acattaccaa	gctcaattac	240
tacatcgctg	actacaaccc	gagcaaactc	accgcaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggctccc	tccttgcacg	ctgggtgccag	tgccggccct	ggcttcacct	360
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gttgcgagcg	tggtcgctgg	gggcgcgtgg	ttgagcggtt	tggagacggc	acgcaaagtc	480
caggctgcgc	ggctgtcctg	cctcgttctt	gaggcgatgg	atcgtgtggg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	gctatcaatg	acctcggcgc	tgctgtggatc	600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatggtg	attccctggg	aagcacaatt	ccatcttggtg	atgagacctc	tgctgtgtgt	780
agaatacagt	cgctgactcc	acatcgctcca	gctgagcgag	gaggttgcaa	gtgcaactcgc	840
ggaactcctt	cccgcattgg	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aagcttgccct	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgccca	ccggtctcag	1080
taatatgtgc	tcggataaga	aagacgggtgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140

tggtgttctc	tcagtgggag	actcgtttct	tagtgggtcat	tccaggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttgttccag	gctcagtgc	cctcaacacc	cccgtcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcggggcggc	gtgttcgaa	1320
gtaaaaaggt	ggtgggttctg	ttaccgacaa	ccttgatatcc	caccttgata	ttttcaccac	1380
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tagtcttcgt	atgggacaag	ccgtgggtggc	gcgaacaagg	cttctcgggc	gtcctccaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatggtc	ggagaccggg	gacggaagt	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtggtcgaa	gcagcagtat	ttccaaggag	1740
cgccgagcgt	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tgttcatttc	gttggaacgg	agacgtcttt	ggtttggaag	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctggtgccag	1920
cagcatag						1928

<210> 42

<211> 598

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 42

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Leu	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Ala
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro
		35				40						45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50				55						60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr
65				70						75				80	
Tyr	Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85					90						95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
		100					105						110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Pro	Phe	Glu	Val	Asp	Ala
	115					120						125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130				135						140				
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145				150						155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165					170						175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Ala	Ile
		180					185						190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
	195					200						205			
Phe	Lys	Leu	Phe	Glu	Arg	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly
	210				215						220				
Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr
225				230						235				240	
Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu
			245					250						255	
Leu	Pro	Ala	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp	Pro
	260					265							270		
Lys	Ala	Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala	His
	275					280						285			
Tyr	Cys	Glu	Lys	Asp	Leu	Ser	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn
	290				295						300				
Gln	Ile	Thr	Arg	Ala	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	
305				310					315					320	


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ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatgggtg attccctgggt aagcacaatt ccatcttgtg atgagacctc tgtcgtgtgt 780
agaatacagt cgctgactcc acatcgcca gctgagcgag gaggttgcaa gtgcactcgc 840
ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgaag accccaaggc 900
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960
aaacttgccct gctgttctcg gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020
agcccacgag atcagcatgt tttttctcac cgactacatc aagagtgcca ccggtctcag 1080
taatattgtc tcggataaga aagacggtgg gcagtatatg cgatgcaaaa caggtgcgtg 1140
tggtgttctc tcagtgggag actcgtttct tagtggtcat tccaggtatg cagtcgcttt 1200
gccatgccat gtcaaaggaa cttgttccag gctcagtgc cctcaacacc cccgtcgcgc 1260
aaattgagca gtcggcatcc ggctgtacag tacgatcggc ctcgggcggc gtgttccgaa 1320
gtaaaaaggt ggtggtttcg ttaccgacaa ccttgatcc caccttgata ttttcaccac 1380
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tagtcttctg atgggacaag ccgtgggtgg gcgaacaagg cttctcgggc gtcctccaat 1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcat cggcaatggt 1560
ccattacctg tttcatggtc ggagaccggg gacggaagtg gtcccaacag tccaagcagg 1620
tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc ggggcccaag 1680
tcccagagcc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag 1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctcagaacgc 1800
cgttcaaggg tgttcatttc gttggaacgg agacgtcttt gggttggaag gggatatg 1860
aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctggtgccag 1920
cagcatag 1928

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<210> 44

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 44

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
1      5      10      15
Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val
20     25     30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35     40     45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50     55     60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65     70     75     80
Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85     90     95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100    105    110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115    120    125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130    135    140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145    150    155    160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165    170    175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
180    185    190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
195    200    205
Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210    215    220
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
225    230    235    240
Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
245    250    255

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Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
 260 265 270
 Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 275 280 285
 Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg
 290 295 300
 Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
 305 310 315 320
 Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
 325 330 335
 Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
 340 345 350
 Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
 355 360 365
 Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
 370 375 380
 Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
 385 390 395 400
 Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 405 410 415
 Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 420 425 430
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 435 440 445
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu
 450 455 460
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 465 470 475 480
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 485 490 495
 Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 500 505 510
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 515 520 525
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
 530 535 540
 Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
 545 550 555 560
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 565 570 575
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 580 585 590

<210> 45
 <211> 1928
 <212> DNA
 <213> Rhinocycladiella atrovirens

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1185)

<400> 45

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cacgtcggcg taggccc aaa cggagggagg tatgtgacaa tagctggaca gattggacaa	120
gacgcttcgg cegtacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaac	180
ctgcgagctt gtcttgctgc agttggagcc acttcaaacy acattaccaa gctcaattac	240
tacatcgctc actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc	300

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tttgcccttg acaggctccc tccttgcaag ctggtgccag tgccggccct ggcttcacct 360
gaatacctct ttgaggttga tgctacggcg ctggttccag gacactcaac cccagacaat 420
gttgcggaag tggctgtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc 480
caggctgcgc ggctgtcctg cctcgttctt gaggcgatgg atcgtgtggg gggaaagact 540
ctgagcgtac aatcggtgcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc 600
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatggtg attccctggt aggcacaatt ccatcttggt atgagacctc tgcgtgtgt 780
agaatacagt cgctgactcc acatcgctca gctgagcgag gaggttgcaa gtgcactcgc 840
ggaactcctt cccgcatggt ctgagctgat cgaagagcat agtcttgaag accccaaggc 900
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960
aaacttgctt gctgttctcg gctgggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020
agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcc a cgggtctcag 1080
taatatgttc tcggataaga aagacggtgg gcagtatatg cgatgcaaaa caggtgcgtg 1140
tggtgttctc tcagtgggag actcgtttct tagtggtcat tccaggtatg cagtcgcttt 1200
gccatgccat gtcaaaggaa cttgttccag gctcagtgc cctcaacacc cccgtcgccg 1260
aaattgagca gtcggcatcc ggctgtacag tacgatcggc ctcggggcggc gtgttccgaa 1320
gtaaaaagggt ggtggtttcg ttaccgacaa ccttgatcc caccttgata ttttcaccac 1380
ctcttccgcg cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga 1440
tagtcttctg atgggacaa ctgtggtggc gcgaacaagg cttctcgggc gtccctcaat 1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcat cggcaatggt 1560
ccattacctg tttcatggtc ggagaccgag gacggaagtg gtccaacag tccaagcagg 1620
tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc gggggccaag 1680
tcccagagcc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag 1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact ggggttcggcg ctcagaacgc 1800
cgttcaagggt tgttcatttc gttggaacgg agacgtcttt ggtttggaag gggatatatg 1860
aaggggcat acgatcgggt cagcgaggcg ctgcagaagt tgtgcctagc ctggtgccag 1920
cagcatag 1928

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<210> 46

<211> 591

<212> PRT

<213> Rhinocycladiella atrovirens

<400> 46

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala
1 5 10 15
Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr
20 25 30
Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala
35 40 45
Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
50 55 60
Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
65 70 75 80
Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
85 90 95
Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
100 105 110
Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
115 120 125
Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val
130 135 140
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
145 150 155 160
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
165 170 175
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
180 185 190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe
195 200 205

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Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
 210 215 220
 Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
 225 230 235 240
 Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
 245 250 255
 Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp
 260 265 270
 Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala
 275 280 285
 His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala
 290 295 300
 Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
 305 310 315 320
 Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
 325 330 335
 Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
 340 345 350
 Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
 355 360 365
 Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
 370 375 380
 Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys
 385 390 395 400
 Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu
 405 410 415
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser
 420 425 430
 Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser
 435 440 445
 Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr
 450 455 460
 Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp
 465 470 475 480
 Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val
 485 490 495
 Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro
 500 505 510
 Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe
 515 520 525
 Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
 530 535 540
 Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
 545 550 555 560
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 565 570 575
 Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala
 580 585 590

<210> 47
 <211> 600
 <212> PRT
 <213> *Exophiala spinifera*

<400> 47
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1 5 10 15
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro

		35					40					45				
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	
	50					55				60						
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr	
65				70					75					80		
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	
				85					90					95		
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	
			100					105					110			
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	
			115					120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	
	130					135						140				
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	
145				150						155					160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	
				165					170					175		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	
			180					185					190			
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	
			195				200					205				
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	
	210					215					220					
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	
225				230						235					240	
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	
				245					250					255		
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	
			260					265					270			
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	
		275					280					285				
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	
	290					295					300					
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	
305				310						315					320	
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	
				325					330					335		
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	
			340					345					350			
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	
		355					360					365				
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	
	370					375					380					
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	
385				390												

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Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530                      535                      540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                      550                      555                      560
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565                      570                      575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580                      585                      590
Val Ala Ser Leu Val Pro Ala Ala
595                      600

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<210> 48
<211> 1392
<212> DNA
<213> Unknown

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<220>
<221> CDS
<222> (1) ... (1392)

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<223> Cys (-) APAO; removal of cysteine 461

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<400> 48
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt      48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1          5                      10                      15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt      96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
          20                      25                      30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg      144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
          35                      40                      45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat      192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50          55                      60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65          70                      75                      80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
          85                      90                      95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag      336
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
          100                     105                     110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg      384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
          115                     120                     125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag      432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130          135                     140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac      480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn

```

145	150	155	160	
ttg cct gct gtt ctc	ggc gta gca aac cag atc aca cgc gct ctg ctc			528
Leu Pro Ala Val	Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
	165	170	175	
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc				576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile				
	180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc				624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly				
	195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc				672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala				
	210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc				720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val				
	225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg				768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser				
	245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc				816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr				
	260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa				864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln				
	275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc				912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe				
	290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc				960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu				
	305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac				1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp				
	325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga				1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly				
	340	345	350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg				1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp				
	355	360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag				1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu				
	370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa				1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln				
	385	390	395	400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	

<210> 49

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<400> 49

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
Leu Glu Thr Ala Arg Lys Val Gln Ala Gly Leu Ser Cys Leu Val	
20 25 30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr	
260 265 270	

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 50
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15

 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30

 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

 ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

 gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056

Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly		
			340					345					350				
cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg		1104
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp		
		355					360					365					
gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag		1152
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu		
		370				375					380						
ccg	gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa		1200
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln		
385					390					395					400		
gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg		1248
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly		
				405					410					415			
tcg	gcg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag		1296
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu		
			420				425						430				
acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggg		1344
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly		
		435				440						445					
caa	cga	ggg	gct	gca	gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca	tag		1392
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	*		
	450					455					460						

<210> 51
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51																	
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly		
1				5					10					15			
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val		
			20					25					30				
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser		
		35					40					45					
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn		
	50					55					60						
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu		
65					70					75					80		
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln		
				85				90						95			
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu		
		100						105					110				
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu		
		115					120					125					
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys		
	130					135					140						
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn		
145					150					155					160		

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Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
210 215 220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

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<210> 52
<211> 1392
<212> DNA
<213> Unknown

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<220>
<221> CDS
<222> (1)...(1392)

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<223> Cys (-) APAO; removal of cysteines 169, 359, and
461

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<400> 52
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt      48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt      96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg      144

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Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser		
		35					40					45					
ggt	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	192	
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn		
	50					55					60						
gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	240	
Asp	Ser	Asn	Gln	Ser		Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu		
	65				70					75					80		
gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	288	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln		
				85					90					95			
gac	ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	336	
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu		
			100					105					110				
gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	384	
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu		
		115					120					125					
atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	432	
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys		
	130					135					140						
cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	480	
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn		
	145				150					155					160		
ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	528	
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu		
				165					170					175			
ggt	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	576	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile		
			180					185					190				
aag	agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	624	
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly		
		195					200					205					
ggg	cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tcg	cat	gcc	672	
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala		
	210					215					220						
atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	720	
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val		
	225				230					235					240		
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	768	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser		
				245					250					255			
ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	816	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr		
			260					265					270				
ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	864	
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln		

275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc			912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc			960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac			1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
	325	330	335
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga			1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
	340	345	350
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg			1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
	355	360	365
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag			1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
	370	375	380
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa			1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
	385	390	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
	405	410	415
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
	420	425	430
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
	435	440	445
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *			
450	455	460	

<210> 53
 <211> 463
 <212> PRT
 <213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

<400> 53

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1	5 10 15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val	
20	25 30

Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35					40				45				
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
	50					55				60					
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65					70					75				80	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85					90					95	
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
			100					105					110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
	130					135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
			165						170					175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala
	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
			245						250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
			260					265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325						330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
			340					345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
		355					360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390					395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
			405						410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
			420					425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
		435					440					445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
	450					455					460				